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## SEQUENCE LISTING

<110> Ishihara Sangyo Kaisha, Ltd.  
<120> Regulation of RAPL-Rap1 Interaction  
<130> IS-08PCT  
<150> JP 2002-316892  
<151> 2002-10-30  
<160> 14  
<170> PatentIn version 3.1  
<210> 1  
<211> 555  
<212> DNA  
<213> Homo sapiens  
<220>  
<221> CDS  
<222> (1)..(555)  
<223> Human Rap1

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gag cag ggc cag aat tta gca aga cag tgg tgt aac tgt gcc ttt tta				432
Glu Gln Gly Gln Asn Leu Ala Arg Gln Trp Cys Asn Cys Ala Phe Leu	130	135	140	
gaa tct tct gca aag tca aag atc aat gtt aat gag ata ttt tat gac				480
Glu Ser Ser Ala Lys Ser Lys Ile Asn Val Asn Glu Ile Phe Tyr Asp	145	150	155	160
ctg gtc aga cag ata aat agg aaa aca cca gtg gaa aag aag aag cct				528
Leu Val Arg Gln Ile Asn Arg Lys Thr Pro Val Glu Lys Lys Lys Pro	165		170	175
aaa aag aaa tca tgt ctg ctg ctc tag				555
Lys Lys Lys Ser Cys Leu Leu Leu	180			
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Met Arg Glu Tyr Lys Leu Val Val Leu Gly Ser Gly Gly Val Gly Lys	1	5	10	15
Ser Ala Leu Thr Val Gln Phe Val Gln Gly Ile Phe Val Glu Lys Tyr	20	25	30	
Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Glu Val Asp Cys	35	40	45	
Gln Gln Cys Met Leu Glu Ile Leu Asp Thr Ala Gly Thr Glu Gln Phe	50	55	60	
Thr Ala Met Arg Asp Leu Tyr Met Lys Asn Gly Gln Gly Phe Ala Leu	65	70	75	80
Val Tyr Ser Ile Thr Ala Gln Ser Thr Phe Asn Asp Leu Gln Asp Leu	85	90	95	
Arg Glu Gln Ile Leu Arg Val Lys Asp Thr Glu Asp Val Pro Met Ile	100	105	110	
Leu Val Gly Asn Lys Cys Asp Leu Glu Asp Glu Arg Val Val Gly Lys	115	120	125	

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<210> 3  
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<212> DNA  
<213> *Homo sapiens*

<220> CDS  
<221> (1)..(798)  
<223> Human RAPL (or Human p30)

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ctg ccc cta gat gcc atc aag cag ctg cac atc agc agc acc acc acc			432
Leu Pro Leu Asp Ala Ile Lys Gln Leu His Ile Ser Ser Thr Thr Thr			
130	135	140	
gtc agt gag gtc atc cag ggg ctg ctc aag aag ttc atg gtt gtg gac			480
Val Ser Glu Val Ile Gln Gly Leu Leu Lys Lys Phe Met Val Val Asp			
145	150	155	160
aat ccc cag aag ttt gca ctt ttt aag cgg ata cac aag gac gga caa			528
Asn Pro Gln Lys Phe Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln			
165	170	175	
gtg ctc ttc cag aaa ctc tcc att gct gac cgc ccc ctc tac ctg cgc			576
Val Leu Phe Gln Lys Leu Ser Ile Ala Asp Arg Pro Leu Tyr Leu Arg			
180	185	190	
ctg ctt gct ggg cct gac acg gag gtc ctc agc ttt gtg cta aag gag			624
Leu Leu Ala Gly Pro Asp Thr Glu Val Leu Ser Phe Val Leu Lys Glu			
195	200	205	
aat gaa act gga gag gta gag tgg gat gcc ttc tcc atc cct gaa ctt			672
Asn Glu Thr Gly Glu Val Glu Trp Asp Ala Phe Ser Ile Pro Glu Leu			
210	215	220	
cag aac ttc cta aca atc ctg gaa aaa gag gag cag gac aaa atc caa			720
Gln Asn Phe Leu Thr Ile Leu Glu Lys Glu Glu Gln Asp Lys Ile Gln			
225	230	235	240
caa gtg caa aag aag tat gac aag ttt agg cag aaa ctg gag gag gcc			768
Gln Val Gln Lys Lys Tyr Asp Lys Phe Arg Gln Lys Leu Glu Glu Ala			
245	250	255	
tta aga gaa tcc cag ggc aaa cct ggg taa			798
Leu Arg Glu Ser Gln Gly Lys Pro Gly			
260	265		

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<211> 265  
<212> PRT  
<213> Homo sapiens

<400> 4

Met Thr Val Asp Ser Ser Met Ser Ser Gly Tyr Cys Ser Leu Asp Glu  
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Glu Leu Glu Asp Cys Phe Phe Thr Ala Lys Thr Thr Phe Phe Arg Asn  
20           25           30

Ala Gln Ser Lys His Leu Ser Lys Asn Val Cys Lys Pro Val Glu Glu  
35           40           45

Thr Gln Arg Pro Pro Thr Leu Gln Glu Ile Lys Gln Lys Ile Asp Ser  
 50 55 60

Tyr Asn Thr Arg Glu Lys Asn Cys Leu Gly Met Lys Leu Ser Glu Asp  
 65 70 75 80

Gly Thr Tyr Thr Gly Phe Ile Lys Val His Leu Lys Leu Arg Arg Pro  
 85 90 95

Val Thr Val Pro Ala Gly Ile Arg Pro Gln Ser Ile Tyr Asp Ala Ile  
 100 105 110

Lys Glu Val Asn Leu Ala Ala Thr Thr Asp Lys Arg Thr Ser Phe Tyr  
 115 120 125

Leu Pro Leu Asp Ala Ile Lys Gln Leu His Ile Ser Ser Thr Thr Thr  
 130 135 140

Val Ser Glu Val Ile Gln Gly Leu Leu Lys Lys Phe Met Val Val Asp  
 145 150 155 160

Asn Pro Gln Lys Phe Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln  
 165 170 175

Val Leu Phe Gln Lys Leu Ser Ile Ala Asp Arg Pro Leu Tyr Leu Arg  
 180 185 190

Leu Leu Ala Gly Pro Asp Thr Glu Val Leu Ser Phe Val Leu Lys Glu  
 195 200 205

Asn Glu Thr Gly Glu Val Glu Trp Asp Ala Phe Ser Ile Pro Glu Leu  
 210 215 220

Gln Asn Phe Leu Thr Ile Leu Glu Lys Glu Glu Gln Asp Lys Ile Gln  
 225 230 235 240

Gln Val Gln Lys Lys Tyr Asp Lys Phe Arg Gln Lys Leu Glu Glu Ala  
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Leu Arg Glu Ser Gln Gly Lys Pro Gly  
 260 265

<212> DNA  
 <213> Homo sapiens

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&lt;221&gt; CDS

&lt;222&gt; (1)..(498)

&lt;223&gt; Dominant-Negative Human RAPL

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1 5 10 15			
ctg gcg gct acc acg gac aag cgg aca tcc ttc tac ctg ccc cta gat			96
Leu Ala Ala Thr Thr Asp Lys Arg Thr Ser Phe Tyr Leu Pro Leu Asp			
20 25 30			
gcc atc aag cag ctg cac atc agc agc acc acc acc gtc agt gag gtc			144
Ala Ile Lys Gln Leu His Ile Ser Ser Thr Thr Val Ser Glu Val			
35 40 45			
atc cag ggg ctg ctc aag aag ttc atg gtt gtg gac aat ccc cag aag			192
Ile Gln Gly Leu Leu Lys Lys Phe Met Val Val Asp Asn Pro Gln Lys			
50 55 60			
ttt gca ctt ttt aag cgg ata cac aag gac gga caa gtg ctc ttc cag			240
Phe Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln Val Leu Phe Gln			
65 70 75 80			
aaa ctc tcc att gct gac cgc ccc ctc tac ctg cgc ctg ctt gct ggg			288
Lys Leu Ser Ile Ala Asp Arg Pro Leu Tyr Leu Arg Leu Leu Ala Gly			
85 90 95			
cct gac acg gag gtc ctc agc ttt gtg cta aag gag aat gaa act gga			336
Pro Asp Thr Glu Val Leu Ser Phe Val Leu Lys Glu Asn Glu Thr Gly			
100 105 110			
gag gta gag tgg gat gcc ttc tcc atc cct gaa ctt cag aac ttc cta			384
Glu Val Glu Trp Asp Ala Phe Ser Ile Pro Glu Leu Gln Asn Phe Leu			
115 120 125			
aca atc ctg gaa aaa gag gag cag gac aaa atc caa caa gtg caa aag			432
Thr Ile Leu Glu Lys Glu Glu Gln Asp Lys Ile Gln Gln Val Gln Lys			
130 135 140			
aag tat gac aag ttt agg cag aaa ctg gag gag gcc tta aga gaa tcc			480
Lys Tyr Asp Lys Phe Arg Gln Lys Leu Glu Glu Ala Leu Arg Glu Ser			
145 150 155 160			
cag ggc aaa cct ggg taa			498
Gln Gly Lys Pro Gly			
165			

&lt;210&gt; . 6

&lt;211&gt; 165

&lt;212&gt; PRT

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<213> Homo sapiens

<400> 6

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Leu Ala Ala Thr Thr Asp Lys Arg Thr Ser Phe Tyr Leu Pro Leu Asp  
20 25 30

Ala Ile Lys Gln Leu His Ile Ser Ser Thr Thr Thr Val Ser Glu Val  
35 40 45

Ile Gln Gly Leu Leu Lys Lys Phe Met Val Val Asp Asn Pro Gln Lys  
50 55 60

Phe Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln Val Leu Phe Gln  
65 70 75 80

Lys Leu Ser Ile Ala Asp Arg Pro Leu Tyr Leu Arg Leu Leu Ala Gly  
85 90 95

Pro Asp Thr Glu Val Leu Ser Phe Val Leu Lys Glu Asn Glu Thr Gly  
100 105 110

Glu Val Glu Trp Asp Ala Phe Ser Ile Pro Glu Leu Gln Asn Phe Leu  
115 120 125

Thr Ile Leu Glu Lys Glu Glu Gln Asp Lys Ile Gln Gln Val Gln Lys  
130 135 140

Lys Tyr Asp Lys Phe Arg Gln Lys Leu Glu Glu Ala Leu Arg Glu Ser  
145 150 155 160

Gln Gly Lys Pro Gly  
165

<210> 7

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<212> DNA

<213> Artificial Sequence

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<223> Nucleotide Sequence for Myc-tag

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<212> PRT  
<213> Artificial Sequence

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<223> Peptide Sequence for Myc-tag

<400> 8

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<210> 9  
<211> 798  
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<213> Mus musculus

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<222> (1)..(798)  
<223> House Mouse RAPL (Region 104 to 901 of mRNA)

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Met Thr Val Asp Ser Ser Met Ser Ser Gly Tyr Cys Ser Leu Asp Glu		
1 5 10 15		
gaa ctg gaa gat tgc ttc ttt acg gct aag acc acc ttc ttc agg aat		96
Glu Leu Glu Asp Cys Phe Phe Thr Ala Lys Thr Thr Phe Phe Arg Asn		
20 25 30		
ctt cag agc aaa cag cct tca aag aat gtc tgt aag gca gtg gag gag		144
Leu Gln Ser Lys Gln Pro Ser Lys Asn Val Cys Lys Ala Val Glu Glu		
35 40 45		
aca cag cac ccg ccc acg ata cag gag atc aag cag aag att gac agc		192
Thr Gln His Pro Pro Thr Ile Gln Glu Ile Lys Gln Lys Ile Asp Ser		
50 55 60		
tat aac agc agg gag aag cac tgc ctg ggc atg aag ctg agt gaa gat		240
Tyr Asn Ser Arg Glu Lys His Cys Leu Gly Met Lys Leu Ser Glu Asp		
65 70 75 80		
ggc acc tac aca ggt ttc atc aaa gtg cat ttg aag ctc cga cgg cca		288
Gly Thr Tyr Thr Gly Phe Ile Lys Val His Leu Lys Leu Arg Arg Pro		
85 90 95		
gtg acg gtg ccc gct ggg atc cgg ccc cag tcc atc tat gat gcc att		336
Val Thr Val Pro Ala Gly Ile Arg Pro Gln Ser Ile Tyr Asp Ala Ile		
100 105 110		
aag gaa gtg aac cct gca gcc acc aca gac aag cgg act tcc ttc tac		384
Lys Glu Val Asn Pro Ala Ala Thr Thr Asp Lys Arg Thr Ser Phe Tyr		

115	120	125		
ctg cca ctc gat gcc atc aag cag cta cat atc agc agc acc acc acc acg Leu Pro Leu Asp Ala Ile Lys Gln Leu His Ile Ser Ser Thr Thr Thr			432	
130	135	140		
gtt agt gag gtc atc cag ggg ctg ctc aag aag ttc atg gtt gtg gac Val Ser Glu Val Ile Gln Gly Leu Leu Lys Lys Phe Met Val Val Asp			480	
145	150	155	160	
aac cca cag aag ttt gca ctt ttt aag cg <sup>g</sup> ata cac aaa gat gga caa Asn Pro Gln Lys Phe Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln			528	
165		170	175	
gtg ctc ttc cag aaa ctc tcc att gct gac tat cct ctc tac ctt cgt Val Leu Phe Gln Lys Leu Ser Ile Ala Asp Tyr Pro Leu Tyr Leu Arg			576	
180	185		190	
ctg ctc gct ggg cct gac acc gat gtt ctc agc ttt gtg cta aag gag Leu Leu Ala Gly Pro Asp Thr Asp Val Leu Ser Phe Val Leu Lys Glu			624	
195	200		205	
aat gaa act gga gag gtg gag tgg gat gcc ttt tcc att cct gaa ctc Asn Glu Thr Gly Glu Val Glu Trp Asp Ala Phe Ser Ile Pro Glu Leu			672	
210	215		220	
cag aac ttt tta act atc ctg gaa aaa gag gag cag gac aag atc cat Gln Asn Phe Leu Thr Ile Leu Glu Lys Glu Glu Gln Asp Lys Ile His			720	
225	230		235	240
caa ctg caa aag aag tac aac aaa ttc cgt cag aaa ctg gaa gag gca Gln Leu Gln Lys Lys Tyr Asn Lys Phe Arg Gln Lys Leu Glu Glu Ala			768	
245		250	255	
tta cga gag tcc caa ggg aag ccg ggg taa Leu Arg Glu Ser Gln Gly Lys Pro Gly			798	
260		265		
<210> 10 <211> 265 <212> PRT <213> Mus musculus				
<400> 10				
Met Thr Val Asp Ser Ser Met Ser Ser Gly Tyr Cys Ser Leu Asp Glu 1 5 10 15				
Glu Leu Glu Asp Cys Phe Phe Thr Ala Lys Thr Thr Phe Phe Arg Asn 20 25 30				
Leu Gln Ser Lys Gln Pro Ser Lys Asn Val Cys Lys Ala Val Glu Glu 35 40 45				

1 0 / 1 1

Thr Gln His Pro Pro Thr Ile Gln Glu Ile Lys Gln Lys Ile Asp Ser  
50 55 60

Tyr Asn Ser Arg Glu Lys His Cys Leu Gly Met Lys Leu Ser Glu Asp  
65 70 75 80

Gly Thr Tyr Thr Gly Phe Ile Lys Val His Leu Lys Leu Arg Arg Pro  
85 90 95

Val Thr Val Pro Ala Gly Ile Arg Pro Gln Ser Ile Tyr Asp Ala Ile  
100 105 110

Lys Glu Val Asn Pro Ala Ala Thr Thr Asp Lys Arg Thr Ser Phe Tyr  
115 120 125

Leu Pro Leu Asp Ala Ile Lys Gln Leu His Ile Ser Ser Thr Thr Thr  
130 135 140

Val Ser Glu Val Ile Gln Gly Leu Leu Lys Lys Phe Met Val Val Asp  
145 150 155 160

Asn Pro Gln Lys Phe Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln  
165 170 175

Val Leu Phe Gln Lys Leu Ser Ile Ala Asp Tyr Pro Leu Tyr Leu Arg  
180 185 190

Leu Leu Ala Gly Pro Asp Thr Asp Val Leu Ser Phe Val Leu Lys Glu  
195 200 205

Asn Glu Thr Gly Glu Val Glu Trp Asp Ala Phe Ser Ile Pro Glu Leu  
210 215 220

Gln Asn Phe Leu Thr Ile Leu Glu Lys Glu Glu Gln Asp Lys Ile His  
225 230 235 240

Gln Leu Gln Lys Lys Tyr Asn Lys Phe Arg Gln Lys Leu Glu Glu Ala  
245 250 255

Leu Arg Glu Ser Gln Gly Lys Pro Gly  
260 265

<210> 11  
<211> 30

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<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Oligonucleotide to act as a primer for PCR  
  
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<212> DNA  
<213> Artificial Sequence  
  
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<223> Oligonucleotide to act as a primer for PCR  
  
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<213> Artificial Sequence  
  
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<223> Oligonucleotide to act as a primer for PCR  
  
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<210> 14  
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<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Oligonucleotide to act as a primer for PCR  
  
<400> 14  
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